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GENETIC VARIABILITY, ASSOCIATION AND DIVERSITY STUDIES IN WHEAT (*TRITICUM AESTIVUM* L.) GERMPLASM

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Abstract

Seventy local and exotic wheat genotypes grown in Faisalabad, Pakistan during the Rabi season of 2005/2006 were evaluated for variability parameters, correlations and path coefficients for eight metric traits i.e., plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility %, 1000 grain weight and yield per plant. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for yield per plant, number of productive tillers per plant and number of grains per spike. The remaining traits recorded moderate to low PCV and GCV estimates. Moderate heritability was observed for number of productive tillers per plant and fertility %. High heritability estimates were recorded for plant height, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and yield per plant. These traits also indicated high genetic advance (except fertility %). Grain yield per plant showed highly significant positive correlation with number of productive tillers per plant, number of spikelets per spike and number of grains per spike and significant positive correlation with spike length. Path coefficient analysis revealed that number of productive tillers per plant and number of grains per spike had the highest direct effect on grain yield per plant and each must be given preference in selection along with optimum plant height to select superior wheat genotypes. The cluster analysis grouped 70 wheat genotypes into 4 different clusters. Five genotypes of China were grouped in cluster I that showed the maximum diversity. Genetic diversity was partially related to the geographic origin. From the cluster mean values, Chinese genotypes deserve consideration for their direct release as a variety(s) or as parents in hybridization programmes to develop high-yielding wheat varieties. The genotypes in cluster II may be used for the improvement of plant height and 1000 grain weight in wheat.

Introduction

Wheat (*Triticum aestivum* L.) is the staple food for a large part of the world population including Pakistan. It is grown on 8307 thousand hectares with total production of 21.708 million tons and an average yield of 2.615 tons/ha (Anon., 2005-2006). This is far below than that of most of the countries of the world like Germany (7.9 tons/ha), France (6.6 tons/ha) and Egypt (6.4 tons/ha).

Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, direct selection for yield as such could be misleading. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield. Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dixet & Dubey, 1984).

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Kumar *et al.,* (2003) reported high heritability coupled with high genetic advance for plant height, number of spikelets per ear, 1000-grain weight and number of days to 50% heading in wheat. The grain yield was significantly and positively correlated with 1000-kernel weight and the number of spikes per square meter (Korkut *et al.,* 2001). Dwivedi *et al.,* (2002) found that total biomass showed the highest direct effect on grain yield which was followed by tillers per plant and grain weight per ear.

The study of associations among various traits is useful to breeders in selecting genotypes possessing groups of desired traits. Hence, in this investigation, exotic as well as local genotypes were used and an attempt was made to generate information on inheritance, relationships of yield and its components and their implication in selection of better genotypes of wheat for the development or improvement of cultivars and germplasm as well.

Materials and Methods

The wheat germplasm consisted of 70 genotypes collected from different National Yield Trials at different locations including eleven exotic lines from CIMMYT. The details of origin/source of selected genotypes are given in Table 1. The experiment was conducted in a randomized block design with three replications at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad during Rabi 2005-2006. Each plot consisted of four rows of 1.0 m length with 30 cm and 15 cm spacing between and within rows, respectively. All the cultural practices were kept constant. Nitrogen was applied @ 85 kg N/ha and phosphorus @ 55 kg P_2O_5/ha before sowing of the crop. Weeds were removed manually as and when required. At maturity five guarded plants from central two rows were selected at random from each plot in each replication for recording data on plant height (cm), number of productive tillers per plant, no. of spikelets per spike, spike length, number of grains per spike, fertility %, 1000 grain weight (g) and yield per plant (g).

The mean data were subjected to analysis of variance to test the level of significance among the genotypes for different characters according to Steel & Torrie (1980). Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, broad sense heritability and correlation coefficients were computed according to the method suggested by Singh & Chaudhary (1985). Genetic advance in terms of percentage of means was estimated as described by Brim *et al*., (1959). The methodology proposed by Dewey & Lu (1959) was used to perform the path analysis for grain yield and its components keeping grain yield as resultant variable and its components as causal variables. Cluster analysis was performed by using the STATISTICA software.

Results and Discussion

a. Genetic variability: Mean squares of plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility %, 1000 grain weight and yield per plant showed highly significant differences between genotypes (Table 1). Such considerable range of variations provided a good opportunity for yield improvement. Genotypic and phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability and genetic advance expressed as percentage of mean for eight characters are presented in Table 3. The estimates of GCV were high for yield per plant (41.19), number of productive tillers per plant (23.79) and number of grains per spike (21.45). The remaining traits recorded moderate to low GCV estimates. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits.

Table 1. Description of seventy wheat genotypes grown in 2005-06.

S. No.	Genotype	Origin	S. No.	Genotype	Origin
1.	Elite 34	CIMMYT	36.	Chakwal 86	PUNJAB
2.	Elite 33	”	37.	FD 83	”
3.	Elite 8	”	38.	TC 4881	”
4.	Elite 73	”	39.	9316	”
5.	Elite 56	”	40.	FD 85	”
6.	Nesser	”	41.	9021	”
7.	Sitta	”	42.	Kohistan 97	”
8.	Elite 88	”	43.	Barani 83	”
9.	Dharwaydy	”	44.	9244	”
10.	Opata	”	45.	6500	”
11.	Weebill-1	”	46.	TC 4884	”
12.	C-228	SINDH	47.	Pak 81	”
13.	Marvi 2000	”	48.	9258	”
14.	CM 24/87	”	49.	6544-6	”
15.	Abadgar	”	50.	9250	”
16.	Soghat 90	”	51.	Rawal 87	”
17.	Kiran 95	”	52.	LU 26-S	”
18.	Sarsabz	”	53.	5039	”
19.	Sindh 81	”	54.	TC 4928	”
20.	Bhittai	”	55.	6529-II	”
21.	QM 4934	”	56.	02013	”
22.	C 591	”	57.	02134	”
23.	NR 234	FEDERAL	58.	02005	”
24.	CH 97	”	59.	03153	”
25.	Marwat 5-01	”	60.	02006	”
26.	Suleman 96	”	61.	02156	”
27.	NR 240	”	62.	03158	”
28.	Margalla 99	”	63.	Pasban 90	”
29.	GA 02	”	64.	Inqlab 91	”
30.	NR 241	”	65.	03156	”
31.	NR 231	”	66.	CA 5033	CHINA
32.	Wafaq 01	”	67.	CA 5039	”
33.	Sarc 1	PUNJAB	68.	Caxui	”
34.	Sarc 2	”	69.	Cayf 3	”
35.	Sarc 5		70.	Caud 24	”

Table 2. Range, mean, mean squares and standard error of means for eight quantitative characters of seventy wheat genotypes.

Character	Range	Mean	Mean squares	Standard error of mean
Plant height	64.57–120.17	91.94	324.832^{**}	2.47
No. of productive tillers /plant	5.33–24.00	9.07	19.557^{**}	1.36
No. of spikelets/spike	8.50–25.67	16.16	20.787^{**}	0.78
Spike length	7.47–17.00	10.25	7.691^{**}	0.49
No. of grains/spike	22.00–85.67	48.45	372.842^{**}	4.02
Fertility %	80.15–97.83	95.47	24.134^{**}	1.41
1000 grain weight	32.3–56.92	41.68	72.506^{**}	0.19
Yield/plant	5.67–36.45	13.34	107.138^{**}	2.35

**Highly significant

Moderate heritability was observed for number of productive tillers per plant and fertility %. High heritability estimates were recorded for plant height, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and yield per plant. Sachan & Singh (2003) also reported high heritability estimates for grain yield, number of spikelets per spike, number of seeds per spike, plant height, 100-seed weight and number of tillers per plant which support the present findings. Heritability and genetic advance are important selection parameters. Heritability estimates alongwith genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al*., 1955). High heritability accompanied with high genetic advance in case of plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and yield per plant indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Similar findings have been reported by Sharma & Garg (2002) and Dwivedi *et al*., (2002). High heritability for fertility % coupled with low genetic advance indicates non-additive gene effects. Therefore, there seems a limited scope for improvement in this trait.

b. Correlation coefficient analysis: The phenotypic and genotypic correlations for morphoagronomic traits are presented in Table 4. Yield per plant had highly significant and positive genotypic and phenotypic correlations with number of productive tillers per plant, number of spikelets and number of grains per spike and significant positive correlations with spike length at both levels. Negative but highly significant to significant genotypic and phenotypic correlations were exhibited by yield per plant with plant height, respectively. It seems logical to select for short stature genotypes for lodging resistance coupled with high yield. The significant positive correlation of tillers per plant and ear length with yield per plant have been reported by Mondal *et al*., (1997) and that of number of grains per spike and number of spikelets per spike by Raut *et al*., (1995). Fertility % and 1000 grain weight showed positive but non significant genotypic and phenotypic correlations with grain yield. Sinha *et al*., (2006) reported positive and non significant genotypic correlation of 1000 grain weight with yield per plant under irrigated timely sown wheat.

The yield components exhibited varying trends of association among themselves. Plant height showed negative and significant to highly significant genotypic correlations with number of productive tillers per plant, number of grains per spike and fertility % and positive significant correlations with 1000 grain weight. Number of productive tillers per plant had highly significant and negative genotypic correlation with plant height, highly significant and significant positive association at phenotypic and genotypic levels, respectively with number of spikelets per spike and number of grains per spike. Number of spikelets per spike exhibited negative significant genotypic correlation with plant height, positive highly significant genotypic and significant phenotypic correlation with number of productive tillers per plant, positive and significant phenotypic correlation with spike length, highly significant and significant positive correlation with number of grains per spike and fertility % respectively, at both levels. Spike length was strongly and positively correlated phenotypically and genotypically with number of grains per spike and positive and significantly with number of spikelets per spike at phenotypic level. Number of grains per spike had strong negative association with plant height and strong positive association with number of tillers per plant, number of spikelets per spike, spike length, number of grains per spike and fertility %. This trait displayed negative and significant genotypic correlation with 1000 grain weight. Fertility % revealed negative and highly significant genotypic and significant phenotypic correlations with both plant height and 1000 grain weight and positive significant and highly significant correlations with number of spikelets per spike and number of grains per spike respectively, at both levels. Thousand grain weight showed significant positive genotypic and phenotypic correlation with plant height, significant negative genotypic correlation with number of grains per spike and negative and highly significant genotypic and significant phenotypic correlation with fertility %.

c. Path coefficient analysis: Path coefficient analysis provides an effective way of finding out direct and indirect sources of correlations. The results are given in Table 5 which reveals that the number of grains per spike exhibited the highest positive direct effect followed by number of productive tillers per plant and 1000 grain weight. Bergale *et al*., (2002) also reported that grains per spikes and tillers per plant had high positive direct effects on grain yield. Direct effect of number of spikelets per spike was negative and moderate. The direct effect of plant height was negligible and its correlation with grain yield per plant was negative and highly significant. The indirect effect *via* number of productive tillers per plant and number of grains per spike was negative and moderate to high. The selection for this trait will not be effective. Number of productive tillers per plant exhibited a high positive direct effect and highly significant correlation coefficient indicating the true relationship therefore direct selection through this trait will be effective for yield improvement. The indirect effect of this trait *via* number of grains per spike was also positive and high. The direct effect of number of spikelets per spike with grain yield was negative however the correlation coefficient was positive due to the positive indirect effects *via* number of productive tillers per plant and number of grains per spike. Since the direct effect was negative, so the direct selection for this trait to improve yield will be undesirable. However, improvement in number of productive tillers per plant and number of grains per spike may help to compensate the negative effect of number of spikelets per spike.

Direct effect was negative and low and correlation coefficient was significantly positive between spike length and grain yield per plant. This was mainly due the indirect positive effect of number of grains per spike and the indirect selection for this trait will be effective to improve yield. The highest positive direct effect and highly significant positive correlation coefficient was recorded between no. of grains per spike and grain yield per plant. The direct selection for this trait will be effective. Dokuyucu & Akkaya (1999) also reported positive direct effect of number of grains per spike and its positive association with grain yield in the Turkish wheat genotypes and these findings support the present results. The indirect effect *via* number of productive tillers per plant was also positive. Direct effect of fertility % was negative with non significant correlation. The selection of this trait will be ineffective. Although, indirect effect *via* number of grains per spike was positive and high and this trait could be selected for yield improvement. Thousand grain weight exhibited positive direct effect with negligible correlation. Selection for this trait will not be rewarding for yield improvement. Aycicek & Yildirim (2006) also reported positive but small direct effects of 1000 grain weight on grain yield in wheat.

Table 6. Mean and standard deviation of four clusters for eight characters.

Characters	Mean ± SD			
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**
Plant height	77.04 ± 10.09	113.18 ± 5.58	92.58 ± 6.38	88.74 ± 6.44
No. of productive tillers /plant	14.87 ± 5.24	8.57 ± 1.42	8.68 ± 1.80	8.60 ± 1.42
No. of spikelets/spike	22.20 ± 2.18	14.33 ± 0.94	17.02 ± 1.49	14.73 ± 1.93
Spike length	11.49 ± 2.03	10.06 ± 1.22	10.63 ± 0.95	9.72 ± 1.93
No. of grains/spike	73.67 ± 9.28	31.14 ± 6.04	53.48 ± 4.92	43.26 ± 4.40
Fertility %	95.63 ± 3.39	89.98 ± 5.76	96.89 ± 0.61	95.36 ± 1.03
1000 grain weight	42.55 ± 3.64	48.55 ± 5.89	41.40 ± 4.01	40.10 ± 4.48
Yield/plant	31.23 ± 4.60	10.73 ± 2.16	13.71 ± 3.39	10.51 ± 2.33

d. Cluster analysis: The analysis of genetic diversity through the cluster analysis has been shown in Fig. 1. Cluster diagram based on Euclidean dissimilarity using complete linkage method categorized the germplasm into four clusters at 30% linkage distance, cluster I consisted five genotypes, cluster II seven and cluster III and IV twenty-nine genotypes each. All the four clusters were analyzed for mean and SD (Table 6). Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits studied. Maximum and minimum genetic distances were observed within cluster I and IV respectively. All the five genotypes of China were grouped in cluster I, six CIMMYT and one genotype of Sindh in cluster II and five of CIMMYT and all genotypes of Pakistan in clusters III and IV. The grouping of CIMMYT and Pakistan wheat genotypes into same clusters (III & IV) indicated the gene flow from CIMMYT to the Pakistan genotypes as most of the Pakistani varieties/lines were developed using CIMMYT germplasm. The CIMMYT genotypes grouped in cluster II may not have been used in Pakistan and therefore were distinct. This analysis shows that there is partial relationship between the geographic origin and their divergence on the basis of all morphoagronomic traits studied. Genetic divergence among wheat genotypes through cluster analysis was also reported by Anjum *et al.*, (2002) and Singh & Dwivedi (2002). The mean number of productive tillers per plant (14.89), number of spikelets per spike (22.20), spike length (11.49), number of grains per spike (73.67) and yield per plant (31.23) were highest in cluster I. The plant height (113.18) and 1000 grain weight (48.55) were maximum in cluster II. It is evident from the results that the accessions in the cluster I i.e., Cayf 3, Caxui, Caud 24, CA 5039, CA 5033 were short stature and high yielding. Therefore these genotypes could be exploited for their direct release as a variety(s) after testing under wider range of environments. Moreover these genotypes can also be used as parents in hybridization programmes to develop high-yielding wheat varieties.

Conclusion

The present study revealed that grain yield per plant had strong and positive genotypic correlation with number of productive tillers per plant and number of grains per spike with maximum direct effects. These two traits were the key contributors to yield per plant suggesting the need of more emphasis on these components for increasing the grain yield in wheat. Number of spikelets per spike and spike length although showed high correlation with grain yield, yet could not be considered in selection criteria due to their low direct effects and high indirect effects *via* number of productive tillers per plant and number of grains per spike.

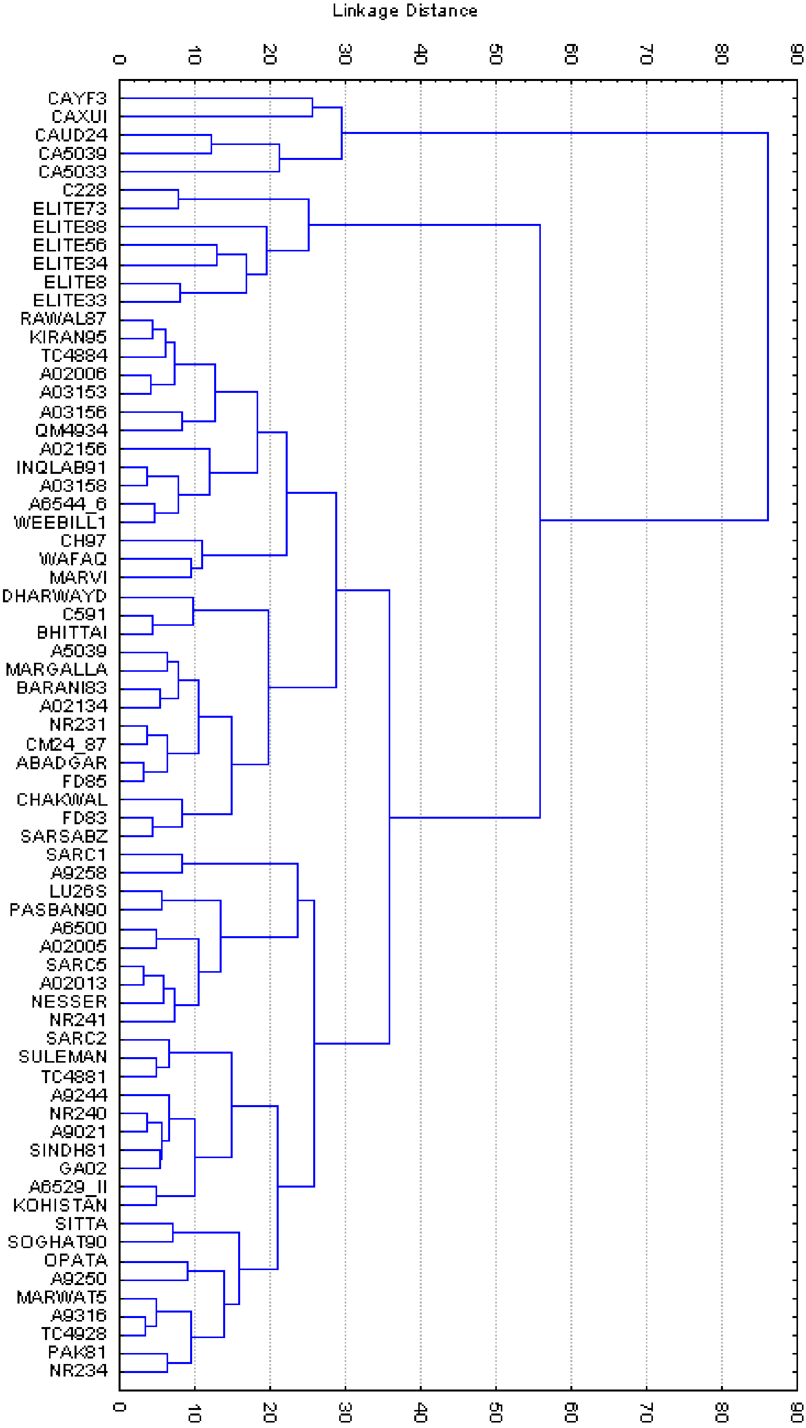

Fig. 1. Cluster diagram of seventy wheat genotypes on the basis of morphoagronomic traits.

Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits. All the five genotypes of China were grouped in cluster I. The mean number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike and yield per plant were highest in this cluster, hence these genotypes may be exploited for their direct release or as parents in hybridization programmes to develop high-yielding wheat varieties. The genotypes in cluster II may be used for the improvement of plant height and 1000 grain weight in wheat.

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